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Mammalia; Eutheria;
                                                                      Golgin-160 (Male-enhanced antigen-2) (MEA-2). GOLGA3 OR MEA2.
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Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil; Alkylation; Multigene family.
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pfam; pF01576; Myosin_tall; 1.
pRINTS; PR0193; MYOSINLEAVY.
proDom; PD000355; myosin_head;
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815
1976
185
701
711
                        Chordata;
         Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%;
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COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 198;
Pred. No. 0.
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    Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1976;
                             Euteleostomi;
         Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND THE SPERMATION: HAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR TESTIS DEVELOPMENT, PROBABLY IDENTICAL WITH THE SEROLOGICALLY DEFECTABLE MALE ANTIGEN (SDM).

1 TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN FOUND IN SPERMATIOS DURING SPERMATOGENESIS. NO EXPRESSION IN LEYDIG CELLS, SPERMATOGONIA, OR SPERMATOCTIES.

1 SIXULARITY: HIGH, TO HUMAN GOLGIN-160.

1 CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE TAYBUT OF THE PROBABLY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN 201 :
SEQUENCE 1325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatogenesis; Developmental protein.
DOMAIN 201 204 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D78270; BAA19612.1; -. HSSP; P18852; 1SCG. MGD; MGI:96958; Golga3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CD-1; TISSUE-Testis; MEDLINE-97217683; PubMed-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                male-enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kondo M., Sutou S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
   935
                                                                                                                     875
                                                            358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLAQEEENVLDA-EFLKNE-----LDSVKAQLSQKDREKR-----DSQAIIDTLRD 109
                                                         HKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQKQPNRTTAESRSSTDVVRI 416
                                                                                                                                                                         HQPPFGDEIDLNTT.
                                                                                                                                                                                                                                                                                        KLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVEMMNPRL 306
   KRLEESNKKLAL - - - - -
                                                                                                                                                                                                                                  QKEMKTKHKAYENA---VSILSRRLQEA---LASKEATDAELNQLRAQSTG--GSSDPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLAVKSNOVEHLOGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLEERNATVESLQNALNKAEMLCSTLKKOM-----KFLEQ-----RODET-----KQ 151
                                                                                                                  HEKIRALEVELQNVGQSKILLEKELQEVITMTSQELEESREKVLELEDELQESRGFRRKI
                                                                                                                                                                                                                                                                                                                                                  RDEMETHLOSLKFDKEQMIALTEANETLKKQTEELQQEAKKATTEQKQKMKRLGSDLTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKATKKRLDSEMKELRQELIKLQGEKKTVEVEHSRLQKDMSLVHQQMAELEGHLQSVQKE 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AREEAHRLKCKMKTMEQIELLLQSQRSEVE----EMIRDMGVGQSAVEQLAVYCVSLKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 POLY-ALA.
; 149880 MW; 3230636962C687B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TATLRKQMQKVKEQFVQQKVMVEAYRRDATSKDQLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 192.5; DB 1;
22.4%; Pred. No. 0.012;
tive 80; Mismatches 156;
                                                                                                                                                                         -----FDVNTPPTQTSGS-QHCLPKKLCLERARSPMQNVLKKV 357
ELEHERGKLTGLGQSNAALREHNSILETALAKREADLVQL
                                                                                                                                                                                                                                                                                                                                                                                                           -LKEA----RKATGELADRLKKDLYSSRSKLKTLNTELDQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          na mouse
ne Golgi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAN
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RESULT 3
MYSN_DROME
ID MYSN_D
AC Q99323

MYSN_DROME Q99323;

STANDARD;

PRT;

2017 A

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Query Match
Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994
01-JUN-1994
16-OCT-2001
                                                            VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                 Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tall; 1.
                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0005634; zip.
InterPro; IPR000048; IQ.
InterPro; IPR00409; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A36014; A36014.
PIR; B36014; B36014.
HSSP; P08799; IMMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin
ZIP.
                                                                                                                                                         DOMAIN
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                  PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; SMART; SM00015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.; "Complete sequence of the Drosophila nonmuscle myosin't transcript: conserved sequences in the myosin tail and splicing in the 5' untranslated sequence."; Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                               DOMAIN
                                                                                                            DOMAIN
                                                                                                                      DOMAIN
                                                                                                                                    DOMAIN
                                                                                                                                              DOMAIN
                                                                                                                                                                       NP_BIND
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                   ATP-binding;
                                                                                                                                                                                                                                PROSITE; PS50096; IQ;
Myosin; Alternative s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90349606; PubMed=2117279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: NOMMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR CELLULARIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) & SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     M35012; AAA28713.1;
                                                                                                                                                                                                                                                        SM00242; MYSc;
  88; Conser
                                                                                   830
886
225
250
682
705
742
1303
1303
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                                                                                                                                                                                                             Calmodulin-L
   Conservative
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                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29,
29,
                                                                                   829
859
2017
232
260
694
727
758
2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Last sequence update)Last annotation update)non-muscle (Zipper protein) (Myosin
           7.9%;
23.8%;
                                                            232016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
  61;
 Score 190; DB
Pred. No. 0.02
61; Mismatches
                                                            ME.
                                                                                                                  ATP.
25 KDA/50 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING
                                                           GLOBULAR TAILPIECE.
MISSING (IN SHORT ISOFORM)
W; 73E3CB02BA8F2528 CRC64
                                                                                           ALPHA-HELICAL TAILPIECE
                                                                                                                                                                             IQ. COILED COIL (POTENTIAL)
                                                                                                                                                                                                        MYOSIN HEAD-LIKE
                                                                                                                                                                                                                               Coiled coil; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
            DB 1;
.025;
 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                       Length 2017;
 Indels
                                                            CRC64
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                                                                                              (LMM).
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 76;
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Gaps
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RESULT 4
MYSC_CHICK
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       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYSC_CHICK P29616;
                                                                                                                                                                                                                                                                                                                                                                                      myosin heavy chain
J. Mol. Fuci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle isoform
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Ver
Archosauria; Aves; Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1592 N--EELEDDL 1599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 65-1102 FROM N.A.
STRAIN-BROILER BREEDERS; TISSUE-Heart;
MEDLINE-92130260; PubMed-1774788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1315
                                                                                                                                                                                                               ++
                                                                                                                                                                                                                                                              "Amino-acid sequence of cardiac muscle myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                 Biol
                                                                                                                                                                                                                                                                                                    Watanabe B.;
                                                                                                                                                                                                                                                                                                                  MEDLINE=93039740;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-259.
                                                                                                                                                                                                                                                                                                                                                                                                                     Jakovcic S., Zak R.;
"Structural and phylogenetic analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329
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ATRIUM. ALSO TRANSIENT EXPRESSION IN SKELETAL MUSCLE DURING FETAL DEVELOPMENT AND REGENERATION FOLLOWING FREEZE INJURY.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEFTAPEFTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN (CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                      1. Chem. Hoppe-Seyler 373:1045-1054(1992).

FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

TISSUE SPECIFICITY: VENTRICULAR MUSCLE AND TRACES LEVELS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTSGSQHCLPKKLCLERARSPMQNVL-----KKVHKVSKP----ESQLS-LGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KATGELADRLKKDLVSSRSKLKTL---NTELDQAKLELRSAQKD----LQSADQEITSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLGLSSKLRQIESEKEALQEQLEEDDEAKRNY---ERKLAEVTTQMQEIKKKAEEDADLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDTLRDTLEER----NATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTIINKLFFDLAQEEENVLDAE--FLKNELDSVKAQLSQKDREKRDSQ------AI
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                                                                                                                                                                                                                                                                                                                  PubMed=1418675;
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Neognathae; Galliformes; Phasian:
                                                                                                                                                                                                                                                                                the short subfragment-2
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isoform (Fragment).
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idae; Phasianinae;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

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01-OCT-1989
16-OCT-2001
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CONFLICT
CONFLICT
                           MYH3
Eukaryota;
              Rattus norvegicus
                                        Myosin
                                                                                                            MYH3_RAT
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ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01576; Myosin_tail; 1.
Myosin; Muscle protein; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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European Bioinformatics Institute. The by non-profit institutions as long
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SIMILARITY: THE P
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                                                                                                                                                                               IDSLQSTLDSEARSRNEAIRL
                                                                                                                                                                                                         -----TAESRSSTDVVRI 416
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                                                                                                                                                                                                                                                                ERARSPMONVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQKQPNRT
                                                                                                                                                                                                                                                                                            ENKNLQEEISDLTNQISEGNKNLH-----
                                                                                                                                                                                                                                                                                                                      TNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCL
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Metazoa;
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                                       chain,
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                                                                                                            STANDARD;
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                                       fast
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%;
                                                     Last sequence update)
Last annotation update
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                                     st annotation update)
skeletal muscle, embryonic
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V -> A (IN REF. 1).
CS -> FAL (IN REF. 1).
H -> Q (IN REF. 1).
T -> R (IN REF. 1).
MW; 2293668D049825DC CR
                                                                                                                                                                                 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 185.5; DB 1; Pred. No. 0.022; 2; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTENTIAL).
Craniata; Vertebrata; Euteleostomi;
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2293668D049825DC CRC64;
                                                                                                            1940 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions
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54 GKKTIINKLFFDLAQEEENV-LDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLE 112

Query Match Best Local S Matches 74

74; Conserv

Conservative

84;

Score 185.5; DB 1; Pred. No. 0.041; 4; Mismatches 180;

Indels Length 1940;

41;

Gaps

7.8%;

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Pfam; PF00612; IQ; 2.head; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; myosin_N; 1.
Pfam; PF01576; myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PFODOM; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                 NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy chain gene. Evidence against intron-dependent evolutio of the rod.";
                                                                                                                                                                                                                                                                                                                       EMBL; X04267; CAA27817.1;
PIR; A24922; A24922.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           Multigene
                                                                                                                                    Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                 Myosin;
                                                                                                                                                                        SMART;
                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                          InterPro; IPR002928;
InterPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-87060988; PubMed-3783701;
                                                        DOMAIN
                                                                                         DOMAIN
                                                                                                      DOMAIN
                                                                                                                DOMAIN
                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strehler E.E., Strehler-Page M.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way find and the first transitions as a long as its content.
                                                                                                                                                            SM00242; MYSC;
E; PS50096; IQ;
                                                                                                                                                                                 SM00015; IQ;
                                                                                                                                          Muscle protein;
                                                                                                                           family.
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223857 N
                                                                                                                                                                                                                                                               myosin_head
                                                                                                                                                                                                                                                                                      Myosin_tail.
                                                                                                                                                                                                                                                                                               Myosin_N
                                                                                                                                                                                                                                                                           Spectrin.
                                                                                                                                                 Coiled coil; Thick filament; Actin-binding,
                                                   IQ.

COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ACTIN-BINDING.

ACTIN-BINDING.
          WW;
         METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
M; B5D546A596E5A696 CRC64;
                                                                                                               MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against intron-dependent evolution
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or send a
                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain; Yam J.W.P., Chan K.W., Hsiao W.L.W.; Suppression of nonmuscle Suppression of transformed phenotype by overexpression of nonmuscle myosin heavy chain-B in p53val135-transformed rat fibroblast."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS, CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JLTO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last annotation
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                 This
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CAPPING.

SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC CHAIN SUBUNITS (MLC-2).

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMMAIN: THE RODLIKE TAIL SEQUENCE IS COMPOSED OF 4 HEPT CHARACTERISTIC FOR ALPHA-HELICAL COTILED COILS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                  IPR000048;
IPR004009;
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a; Chordata;
               Myosin_N
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16-OCT-2001
Myosin II he
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SMART; SM00242; MYSC;
PROSITE; PS50096; IQ;
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pfam; PF01577; Myosin_tail; 1.
priNTs; PR00193; MYOSINLEAVY.
proDom; PD000355; myosin_head;
                                                                                                                                   Eukaryota; Mycetozoa; NCBI_TaxID=44689;
                                                                                                                                                Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
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                                                            Dictyostelium
                                                                                                                                                                                                                        01-NOV-1988
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InterPro; IPR001609;
MEDLINE=90353583; PubMed=2387408;
            STRAIN-AX2
                                                           "Conserved protein domains in a myosin Dictyostelium discoideum.";
                                                                                   Warrick H.M., de Lozanne A., Leinwand
                                                                                                SEQUENCE FROM N.A. MEDLINE=87092266;
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                        PHOSPHORYLATION SITES, AND MUTAGENESIS
                                                 Proc.
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77; Conser
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                                                                                                                                                                                   heavy chain, non
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845
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(Rel. 40, Last ann
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22.1%;
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COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

MW; E32708BF9BF2B470 CRC64;
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Pred. No. 0.
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                                                                                     L.A.,
                                                                                                                                                Dictyostelium
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Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;
"X-ray crystal structure and solution fluorescence characterization of Mg.2'(3')-0-(N-methylanthraniloy!) nucleotides bound to the Dictyostelium discoideum myosin motor domain.";

J. Mol. Biol. 274:394-407(1997).

-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.

-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALING THE ACTIVITY THAT BINDS TO ACTIVE THAT BINDS TO ACTIVE ASSEMBLES INTO FILAMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith C.A., Rayment I.; "X-ray structure of the magnesium(II).ADP.vanadate complex of the "X-ray structure of the magnesium otor domain to 1.9-A resolution."; Biochemistry 35:5404-5417(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagle G., Noegel A., Scheel J., Gerisch "Phosphorylation of threonine residues of Dictyostelium myosin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Replacement of threonine resphosphorylatable heavy chain FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE-98070605; PubMed-9405148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=95345066; PubMed=7619795;
Fisher A.J., Smith C.A., Thoden J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry
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MEDLINE=97452580; PubMed=9305951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96206189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "X-ray structure of the magnesium(II)-pyrophosphate complex of truncated head of Dictyostelium discoideum myosin to 2.7-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith C.A., Raymen
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MEDLINE=95345067; PubMed=7619796;
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Gerisch G.;
                                                                                                                                                                                                                                                                                                                                                                                                                             lick A.M., Bauer C.B., Thoden J.B., Rayment I.;
-ray structures of the MgAPP, MgATPgammaS, and MgAMP
the Dictyostelium discoideum myosin motor domain.";
ochemistry 36:11619-11628(1997).
                                    PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT THE ACTIN-ACTIVATED ATPASE ACTIVITY.
MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO ACTIVITY. PERHAPS CORRELATED WITH THE ABSENCE POSITION (688).
          SIMILARITY:
SIMILARITY:
                                                                                                        DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                  MEROMYOSIN (LMM) AND 1 HEAVY MEROMY SPLIT INTO 2 GLOBULAR SUBFRAGMENTS SUBFRAGMENT (S2).
                                                                                                                                                                                            DOMAIN:
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InterPro; IPR001609; myosin_he
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S00250; S00250.

IMMA; 03-DEC-97.

IMMD; 17-AUG-96.

IMMN; 03-DEC-97.

IMMN; 03-DEC-97.

IMMN; 03-DEC-97.

IMMN; 03-DEC-97.
KKVHKVSKPESQLSLGGQRCVGELDEE
                  A----ANKKLQ---
                                                                                           --EELEEMKR-VNDGQSDTISRLEKIKDELQKEVEELTES----FSEESKDKGVLEKT
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                                   SPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVL
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2 P11055; Q15492;

T 01-JUL-1989 (Rel. 11, Created)

T 01-JUL-1989 (Rel. 11, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Myosin heavy chain, fast skeletal muscle, emb
                                                                                                                                                                                                                                        Rarsch-Mizrachi I., Travis m., Line Rarsch-Mizrachi I., Travis m., Line Rarsch-Mizrachi I., Travis m., Line Rarsch-Mizrachi II., Travis m., Line Rarsch-Mizrachi A. Sequence analysis of a human embryonic sketch muscle myosin heavy chain gene. "."

Nucleic Acids Res. 17:6167-6179(1989).

-!- FUNCTION: MUSCLE CONTRACTION.

-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-!- DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL MICH.

-!- DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN HEART AND ADULT SKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eller M.S., Stedman H.H., Sylvester J.E., Rubinstein N.A., Kelly A.M., Sarkar S.; "Nucleotide sequence of full length human chain cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYH3.
Homo sapiens (Human).
Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eller M.S., Stedman H.H., Sylvester J.E., Raychowdhury M.K., Rubinstein N.A., Kelly "Human embryonic myosin heavy chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=89263803; PubMed=2726495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Karsch-Mizrachi I.
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MEDLINE=90235862; PubMed=1691980;
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                                                                                                        DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDE: CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                            SUBFRAGMENT (S2)
 SWISS-PROT entry is copyright. It is produced een the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are a
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., Travis M., Blau H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                          1439
                                                                                                                                                     1382
                                                                                                                                                                                                1322
                                                                                                                                                                                                                                          1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X13988; CAA32167.1; -. EMBL; X13100; CAA31492.1; -. EMBL; X51593; CAA35942.1; -. EMBL; X15696; CAA33731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   мyosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002928; InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                           173
                                                                                                                                                                                                                     113
  398
                                                                                                                                221
                                                                                      281
                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; P08799; 1MMD
160720; -.
                                                                                                                                                                                                                                                            GKKTIINKLFFDLAQEEENV-LDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S04090;
                     DIQLALEEAEAALEHEEAKILRIQLELTQVKSEIDRKIAEKDEEIEQLKRNYQRTV---E
                                                                                                                                                                                                                                        GKNEETQRSLSELTTQKSRLQTEAGELSRQLEEKESIVSQLSRSKQAFTQQTEELKRQLE 1321
 KQPNRTTAESRSSTDVVRI 416
                                                               VKRENKNLEQETADLTEQTAENGKTIHE
                                                                              ASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK-
                                                                                                         LAAALDKKQRNFDKVLAEWKTKCEESQAELEASLKESRSLSTELFKLKNAYEEALDQLET
                                                                                                                              LADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQETTSLRKKSDDPPGNLEP
                                                                                                                                                    QRTEELEEAKKKLAQRLQD----SEEQVEAVNAKCASLEKTKQRLQGEVEDLMVDVERANS
                                                                                                                                                                                               EENKAKNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAI
                                                                                                                                                                                                                  ERNATVESLQNALNKAEMLCSTLKKOMKFLEQRODETKQAREEAHRLKCKMKTMEQIELL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00015; IQ;
                                  -KLCLERARSPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscle protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50096; IQ;
                                                                                                                                                                        -LQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKK-----EYENLKEARKATGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000048;
IPR004009;
                                                                                                                                                                                                                                                                                                                                         1331
1391
1608
1663
1940
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                              840
179
656
758
130
696
706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S04090.
                                                                                                                                                                                                                                                                                                                                        ΑĄ;
                                                                                                                                                                                                                                                                                                                                                  781
811
1933
186
678
772
130
696
706
1331
1332
1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IQ.
; Myosin_N.
; Myosin_tail.
; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding;
                                                                                                                                                                                                                                                                                              7.7%;
19.5%;
                                                                                                                                                                                                                                                                                                                                        224035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coiled coil; Thick filament;
                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                                      KK -> QE (IN REF. 1 AN SR -> RA (IN REF. 3). RG -> QT (IN REF. 2). WW; 43CA58C6A4BA1253 C
                                                                                                                                                                                                                                                                                                                                         ¥
(¥,
                                                                                                                                                                                                                                                                                  Score 184.5; DE
Pred. No. 0.046;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                 ALKYLATION (SH-2
A -> G (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQ.
COILED COIL (POTENTIAL)
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                       METHYLATION (TRI-)
ALKYLATION (SH-1)
                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NISOYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEAD-LIKE
                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                    179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                    Indels
                                                               -LEKSRKQIELEKA
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                                                                                                                                                                                                                                                                                                                                                                        2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                         1940;
                                                                                                                                                                                                                                                                                   41;
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                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 commercial
                     1596
                                                                                                          1498
                                                                                                                                                    1438
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                                                               1539
                                                                                                                                                                        220
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AC P24733;

DT 01-MAR-1992 (
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                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Adductor muscle;

MEDLINE-92011595; PubMed-1917970;

Myitray L., Goodwin E.B., Szent-Gyoergyi A.G.;

"Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation.";

J. Biol. Chem. 266:18469-18476(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Adductor muscle;
MEDLINE-9108319; PubMed-2263488;
Nyitray L., Goodwin E.B., Szent-Gyorgyi
"Nucleotide sequence of full length cDNN
muscle myosin heavy chain ";
muscle myosin heavy chain ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, striated muscle.
Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resolution: implications for Structure 4:21-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of the regulatory domain of scallop myosin resolution: implications for regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houdusse A., Cohen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96419133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:306-312(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of the regulatory domain of scallop myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Szent-Gyorgyi A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
MEDLINE-94173332; PubMed-8127365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=31199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pectinoidea; Pectinidae;
                                                              L; X55714; CAA39247.1;

$13557; $13557.

$440997; A40997; A40997;

$1SCM; 30-APR-94.

$1MDC; 11-JUL-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: MUSCLE CONTRACTION.

FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAP EURCTION: MYOSIN IS A PROTEIN THAT EN ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSI: HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS.

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS.

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harrison D.H., Schlichting I., yorgyi A.G., Cohen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acids Res. 18:7158-7158(1990)
      IPR000048;
IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed-8805510;
   Myosin_N
                                  ĮQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (2.0 ANGSTROMS) OF 777-836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Argopecten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sweet R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNITS
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MYSU_RABIT Q99105; Q1-JUN-1994 01-JUN-1994 15-JUL-1998

(Rel. (Rel. (Rel.

29, Created)29, Last sequence update)36, Last annotation update)

Myosin

heavy

chain,

embryonic smooth muscle isoform (Fragment).

RESULT 10

STANDARD;

PRT;

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Best Local
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  1271
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
NP_BIND
NOD_RES
MOD_RES
HELIX
TURN
HELIX
TURN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head;
Pfam; PF02736; Myosin_tail;
Pfam; PF01576; Myosin_tail;
PRINTS; PR00193; MYOSINHEAVY
                                                                                      1196
                                                                                                                                 1137
                                                                                                                                                                           1077
                                                                                                                                                                                                                     1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin; Musca
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00015; IQ; 1. SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00193; MYOSINHEAVY ProDom; PD000355; myosin_heav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002928;
InterPro; IPR002017;
                      389
                                                                335
                                                                                                           275
                                                                                                                                                     233
                                                                                                                                                                                                                                                               963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001609;
                                                                                                                                                                                               184
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                     FIRNAVLGQKQPNRTTAESRSST
                                                                                                                                                                                                                                                                                                                             KKTIINKLFFD------LAQEEENVLDAEFLKNELDSVKAQL------SQ
                                                                                                                               NRELEELGERLDEAGGATSAQIELNKKREAELLKIRRDLEEASLQHEAQISALRKKHQD-
                                                                                                                                                                                                                                      EMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMK-----TMEQIELLLQSQRSEVEEM 183
                                                                                                                                                                                                                                                               QDKAHKDNQ--ISTLQGEISQQDEHIGKLNKEKKALEEANKKTSDSLQAEEDKCNHLNK-
                                                                                                                                                                                                                                                                                   KDREKRDSQAIIDTL-----NALNKA 128
                                                                                                                                                                                                                                                                                                        EKLIMQKADFESQIKELEERLLDEEDAAADLEGIKKKMEADNANLKKDIGDLENTLQKAE
                                                                HCLPKKLCLERARSPMQNVLKKVHKVSKPESQLS-----LGGQRCVGELDEELAGAFPL
                                                                                                        PGNLEPASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQ
                                                                                                                                                                          VRRKEAEISSLNSKLEDEQNLVSQLQRKIKELQARIEELEEELEAERNARAKVEKQRAEL
                                                                                                                                                                                                                    --LKAKLEQALDELEDNLEREKKVRGDVEKAKRKVEQDLKSTQENVEDLERVKR-ELEEN
                                                                                                                                                   RSKLKTLNTELDQA-----KLELRSAQKDLQSA----DQEITSLRKKSDDP
                                                                                                                                                                                              102;
                                                                                                                                                                                                                                                                                                                                                  Similarity 23.(
02; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              778
836
836
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703
                                                                                      -AANEMADQV-----DQLQKVKSKLEK----DKKDLKREMD-----DLESQMT
QSQKSRLQAENSDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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Spectrin.
                                                                                                                                                                                                                                                                                                                                                              23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                        222821 MW;
                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>-</u>
                      411
                                                                                                                                                                                                                                                                                                                                                             Score 183;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SII
ALKYLATION (SH-2) (BY SII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RODLIKE TAIL (S2
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01576; Myosin_tail;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A38650; A38650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10280; BAA01124.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arteriosclerosis
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                 150
                                                                                                                                                                                                                                                                                                                                                                               128
260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MET C-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED OF CONSED OF CHARACTERISTIC FOR ALPHA-HELICAL COILED ON THE STATE INTO 1 LIGHT
MEROMYOSIN (LAM) AND 1 HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HWM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration wheen the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on in by non-profit institutions as long as its content is in no waitified and this statement is not removed. Usage by and for commercial contents is the statement is not removed.
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SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC WHICH DICTATE THE ALPHA-HELICAL COILED-COIL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNK 127
                                                                                                                                                                                                              DLKDLEAQIEAANK----ARERRVKQLRRLQAQMKDYQRELEEARGSRDEIFAQSKE----
                                                                                                                                                                                                                                                                                                                                                                          AEMLCSTLKKQMKFLEQRQDE-----TKQAREEAHRLKCKMK-----TMEQIEL 171
EARMRQLEEELEEEQSNMELLNDRFRK----
                                                                                                     SEKKLKSLEAEILQLQEELASSERARRHAEQERDEL---ADEIANSASGKSALLDEKRRL
                                                                                                                                                        SRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRL
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                                                ----VFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                501 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58118 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.6%;
22.0%;
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COILED COIL (POTENTIAL).
; 49F793247D00973E CRC64;
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TTLQVDTLNAELAAERSAAQKSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141;
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Pfam;

PF00612; IQ; 2.
PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.

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MYHD_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The chunan extraocular muscle myosin heavy chain gene (MYH13) maps to rethe cluster of fast and developmental myosin genes on chromosome 17."; Genomics 54:188-189(1998).

C: -: FUNCTION: MUSCLE CONTRACTION.

C: -: FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 CHEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

C: -: SUBCULTURAR LOCATION: Thick filaments of the myofibrils.

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                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99026150; PubMed=9806854;
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MEDLINE=99318869; PubMed=1
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, extraocu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Winters L.M., Briggs M.M.,
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       InterPro;
                                 InterPro;
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                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFRAGMENT (S2)
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                                                                                                                                                  603487;
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l. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095252;
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IPR004009;
IPR002928;
IPR001609;
                                                                                                                IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                             Swiss Institute of Bioinformatics and the E
Bioinformatics Institute. There are no rest
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Myosin_N.
Myosin_tail.
myosin_head.
                                                                                                                IQ.
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Best Local s
Matches 84
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P12844;
01-OCT-1989 (
01-OCT-1989 (
16-OCT-2001 (
Myosin heavy
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NP_BIND
DOMAIN
DOMAIN
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                   CAEEL
                                                 SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=89178677; PubMed=2926820;
                                                                                           Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
     heavy chain gene family.";
J. Mol. Biol. 205:603-613(1989).
                          Dibb N.J., Maruyama I.N., Krause M., "Sequence analysis of the complete C
                                                                                                                            Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                       1545
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SMART; SM00242; MYSC;
                                                                                                                                        MYO-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                        C---
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                                                                                                                                                                                                                                                                                 IRNAVLGQKQPNRTT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
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9 (Rel. 12, Last
1 (Rel. 40, Last
vy chain A (MHC)
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179
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709
1938
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814
1938
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681
775
130
699
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                                                                                                                                                  A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYOSIN HEAD-LIKE.

1Q.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 180;
Pred. No. 0.
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                 -AESRSSTDVVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methylation;
                           Caenorhabditis
                                                                                                                                                           on update)
                                                                                                                                                                                                       1969
                                     Karn
                                                                                                                                                                                                                                                                                                                                                                                                                DOAKLELRSAOKDLOSADOEITSLRK
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.076;
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                                      4
                                                                                                                  Rhabditida;
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                           elegans myosin
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                                                                                                                  Rhabditoidea;
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Best Local
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Pfam; PF00612; TQ; 1.
Pfam; PF00263; myosin_head; 1.
Pfam; PF01576; myosin_tall; 1.
Pfam; PF01576; myosin_tall; 1.
Pfam; PF01576; myosin_head; 1.
PRINTS; PR00193; myosin_head; 1.
SMART; SM00015; TQ; 1.
SMART; SM00042; MYSS; 1.
                                                                                                                                                                                                                               NP_BIND
DOMAIN
DOMAIN
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: MUSCLE CONTRACTION.

-i- SUBUNIT: MUSCLE EXYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELLCAL COILED COILS.
-i- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-i- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X08067; CAA30856.1; -. PIR; S02771; S02771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002928; Myosin_tail.
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                                             929
                                                                                                    872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000048;
                119
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                                                                                                                               31 LOCLIOWFETAPSRTCPQCRIQVGKKTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIV WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THIC SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY C.ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFRAGMENT
            ESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRS
                                                                                                    LEEAVQRGEIARSQLESQVADLVEEK --
                                          ESKLSDITGQLEDMQERNEDLARQKKKTDQELSDTKKHVQDLELSLRKAEQEKQSRDHNI
                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                             Muscle
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857
179
667
770
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                              Methylation;
                                                                                                                                                                                                                                                                                                                                                                                             protein;
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689
784
130
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21.2%;
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                                                                                                                                                                                                                                  225509
                                                                                                                                                                                                                                                                                                                                                                             Coiled coil; Thick filament; Actin-binding; n; Alkylation; Multigene family.
                                                                                                                                                            85;
                                                                      DREKRDSQAIIDT ---
                                                                                                                                                                                                                               IQ.
COLLED COIL (POTENTIAL).
ATP.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                  MW.
                                                                                                                                                                         Score 180; DB 1; Pred. No. 0.077;
                                                                                                                                                                                                                                                                                                                                                               MYOSIN
                                                                                                                                                            Mismatches
                                                                                                   NALFLSLETEKANLADAEERNEKLNQLKATL
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                                                                                                                                                                                                                                                                                                                                                               HEAD-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                       Length 1969;
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                                                                     LRDTLEE---RNATV
                                                                                                                                                            Indels 180;
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O1-JUN-1994 (Rel. 29, o
O1-FEB-1996 (Rel. 33, i
16-OCT-2001 (Rel. 40, i
Myosin heavy chain, noi
                                                                                                                                                                                                                                                                                                              Circ
                                                                                                                                                                                                                                                                                                                        MEDLINE-91316803; PubMed-1860190;
Simons M., Wang M., McBride O.W., Kav
Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains
on different chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phillips C.L., Yamakawa K., Adelstein R.S.;

"Cloning of the cDNA encoding human nonmuscle myosin heavy
analysis of human tissues with isoform-specific antibodies.
J. Muscle Res. Cell Motil. 16:379-389(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 63-722 FROM N.A
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MEDLINE=96025307; PubMed=7499478;
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                                                                                 CAPPING.

CHAPNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2),

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELLA COILED CHARACTERISTIC CHARACTERISTIC FOR ALPHA-HELLA COILED CHARACTERISTIC FOR ALPHA-HELLA COILED CHARACTERI
                                              SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR SIMILARITY: CONTAINS 1 IQ DOMAIN.
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    SWISS-PROT entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GRTKFIQPR-----DTTIIRPVPVKSKAKSKQKVRIKTVSSASQPKLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQALAATAKNLEHENTILRE----HLDEEAESKADLTRQISKLNAEIQQWKARFDSEGLN
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nonmuscle type B (Cellular myosin
myosin heavy chain-B) (NMMHC-B).
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01578; MYOSINHEAVY.
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InterPro;
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                                                                  RL-----VFESPAPVEMMNPRLHOPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK
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                    KLCLERARSPMQNVLKKVHKVSKPESQLSLGG-QRCVGELDEEL
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Myosin_N.
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21.8%;
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COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             X.
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                                                                                                                                                                                                                                                                                                                                                                                                                MYOSIN HEAD-LIKE
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J. Cell
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
        965
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Submitted (MAY-1996) to
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Kendrick K.E.;
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                                                                    56 KTIINKLEEDLAQEEENVLDA-EFLKNE----LDSVKAQLSQKDREKRDSQAIIDTLRDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                '; P80220; IDIP.
S0002216; USO1.
PPro; IPR002017;
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Biol. 113:245-260(1991).
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ta A., Ogawa Y.,
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COLLED COIL (POTENTIAL).
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Pred. No. 0.087;
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Query Match Best Local S Matches 74

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Hypothetical SEQUENCE 1
                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-OCT-1996 (Rel. 34, Last sence)
01-OCT-1996 (Rel. 34, Last and
Hypothetical 222.8 kDa protein
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                                                          EMBL; Z70690; CAA94624.1;
                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
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      RA Bagguley C., Bailey J., Ballow K., Battle K.N., Beasley O., Bridgeman A.M., Buck D., Burryess J., Burrill W.D.,
RA Blakey S., Bridgeman A.M., Buck D., Burryess J., Burrill W.D.,
RA Burton J., Carder C., Carter N.P., Chenry, Clark G., Clegg S.M.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Collie G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Collie G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Collie G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
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RA Collie G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.J.,
RA Collie G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.J.,
RA Kimberley A., King A., Laird G.K., Langford C.F., Levershaw J.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Milley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Milley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Milley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Beck S., Rogers J., Shintizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA Beck S., Rogers J., Shintiani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
RA Muller T., Danman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Muller T., Danman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Muller T., Danman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Muller T., Danman A., Fang G., Chissoe S., Murray J., Miller N.,
RA Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P.,
RA Hawkins J., Handid H., Shikh T., Kurahashi 
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P35579; O60805;
01-JUN-1994 (Rel
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Mammalia; Eutheria;
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  Shizuya H.,
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  Simon
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  Dumanski J.P
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CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2

CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

POMALIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC BAY HARACTOR FOR AND LEUKOCYTE INCLUSIONS.

CHARACTERISTIC FOR ALPHA-HELETS AND LEUKOCYTE INCLUSIONS.

BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

WITH ADDITIONAL ALPORT-LIKE CLINICAL FEATURES OF SENSORINEURAL DEAFNESS, CATARACTS AND AEPHRITIS.

DEAFNESS, CATARACTS AND AEPHRITIS.
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SEQUENCE OF 714-1960 FROM N.A.
SEQUENCE OF 714-1960 FROM N.A.
MEDLINE-90138958; PubMed=1967836;
Saez C.G., Myers J.C., Shows T.B., Leinwand L.A.;
"Human nonmuscle myosin heavy chain mRNA: generat through alternative polyadenylylation.";
through alternative polyadenylylation.";
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"The DNA sequence of human chromosome 22.";
Nature 103.100-100-100-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human nonmuscle myosin heavy chains on different chromosomes."; Circ. Res. 69:530-539(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iolascon A., Zelante L.L., Savoia A., Balduini C.L., Noris P., Magrini U., Belletti S., Heath K.E., Babock M., Glucksman M.J., Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.; "Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and "Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and Sebastian syndromes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seri M., Cusano M., Gangarossa S., Caridi G.,
Ghiggeri G.M., Ravazzolo R., Savino M., Del V
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O'Brien K.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                           May-Hegglin anomaly.";
Nat. Genet. 26:106-108(2000).
-!- FUNCTION: CELLULAR MYOSIN
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"Mutation of MYH9, encoding non-muscle myosin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS MHA ILE-1155 AND LYS-1841.
MEDLINE=20428193; PubMed=10973260;
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CAUSE OF

SEBASTIAN SYNDROME

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InterPro; IPRO00048; IQ.
InterPro; IPRO04009; Myosin_N.
InterPro; IPRO04009; Myosin_tail.
InterPro; IPRO02928; Myosin_tail.
InterPro; IPRO02017; Spectrin.
InterPro; IPRO01609; myosin_head.
Pfam; PF00612; IQ; 1.
Pfam; PF00736; Myosin_head; 1.
Pfam; PF02736; Myosin_kail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; Myosin_head; 1.
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L; M81105; AAA59888.1; -.
M69180; AAA61765.1; -.
L; M31013; AAA63349.1; -.
P; P08799; ILVK.
; 160775; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SBS), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS. DISEASE: DEFECTS IN MYH9 ARE THE CAUSE OF AN AUTOSOMAL DOMINANT FORM OF NONSYNDROMIC SENSORINEURAL DEAFNESS (DENAIT) WHICH IS CHARACTERIZED BY PROGRESSIVE HEARING IMPAIRMENT AND
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155100;
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E -> K (IN MHA).

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STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDLINE-20570466; PubMed-11121031;

MEDLINE-20570466; PubMed-11121031;

MEDLINE-20570466; PubMed-11121031;

MEDLINE-20570466; PubMed-11121031;

Makino S.-I., Higuchi S.,

Kawashima - Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamot Kawamot Munoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by genomic "Archaeal adaptation to higher temperatures sequence of Thermoplasma volcanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

-!- FUNCTION: Involved in DNA double-strand break repair (DSBR).
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                                                                                                                                                                                     Thermoplasma
                                                                                                                                                                                                 Archaea; Euryarchaeota;
                                                                                                                                                                                                                Thermoplasma volcanium
                                                                                                                                                                                                                                                          16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                    444
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Local Similarity
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rad50/mrell complex possesses
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TEDAKLRLEV-----NLQAMKAQFERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKLCLERA----RSPMQNVL-----KKVHKVSKPESQLSLGGQRC---VGELDEELAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFPLFIRNAVLGOKQPNRTTAESRSSTDVVRIGFDGLGGRTKFIQPRDTTIIRPV-PVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKAELERLNKQFRTEMEDLMSSKDDVGKSVHELEKSKRALEQQVEEMKTQLEELEDELQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HQRQSACNLEKKQKKFDQLLAEEKTISAKYAEERDRAEAEAREKETKALSLARALEEAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKMEDSVGCLETAEEVKRKLQKDLEGLSQRHEEKVAAYDKLEKTKTRLQQELDDLLVDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKSDDPPGNLEPASATN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDTQELLQEENRQKLSLSTKLKQVEDEKNSFREQLEEEEEAKHNLEKQIATLHAQVADMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEMIRDMGV----GQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQ------QIELLLQS-------QRSEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELKMQLAKKE---EELQAALARVEEEEAAQKNMALKKIRELESQISELQEDLESERASRNKA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAQLQELQVKFNEGERVRTELADKVTKLQVELDNVTGLLSQSDSKSSKLTKDFSALESQL
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                                                                                                                                                                                                                                                                                                                  STANDARD;
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40, Last sequence update)
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40, Last annotation defacts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226531 MW;
                                                                                                                                                                                                 Thermoplasmales; Thermoplasmaceae;
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                                                                                                                                                                                                                                                                                                                                                                                        1618
                                                                                                                                                                                                                                                                                                                                                                                                                    465
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        588F84BB8C106E6F CRC64
single-strand endonuclease activity
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.11;
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                                                                                   Kawamoto
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Best Local
                                                          N_ACACA

MYSN_ACACA

STANDARD;
P05659;
01-NOV-1988 (Rel. 09, Cr
01-NOV-1988 (Rel. 09, La
16-OCT-2001 (Rel. 40, La
16-OCT-2011 (Rel. 40, La
Myosin II heavy chain, n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete NP_BIND 30 37 ATP (BY SIMILARITY).

DOMAIN 171 737 COILED COIL (POTENTIAL).
SEQUENCE 895 AA; 103223 MW; 4A47DA9287E82D3A CRC64;
Acanthamoeba castellanii (A
Eukaryota; Acanthamoebidae;
NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003439; ABC_transportr.
InterPro; IPR000875; Cecropin.
InterPro; IPR001238; RecF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP000991; BAB59370.1; -.
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                                                                                                                                                                                                                     447
                                                                                                                                                                                                                                                                                411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SUBUNIT: Forms a con
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and ATP-dependent double-strand-specific exonuclease activity Rad50 provides an ATP-dependent control of mre11 by unwinding and/or repositioning DNA ends into the mre11 active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                LSLGGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNINKDVFLTSIFVRQGEMDALVSKDPAERKKILDEILNIDRLEAGYLLLKEVIDDLTAN 181
                                                                                                                                                                                                                   AMLSGR
                                                                                                                                                                                                                                                                                                           HQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVLKKVHKVSKPESQ
                                                                                                                                                                                                                                                                                                                                         RSSLKEDEDNYQSAVRNIENIKKWIENEEKEIERMSAFISEILKIQEITP--
                                                                                                                                                                                                                                                                                                                                                            KLELRSAQKDLQSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVEMMNPRL
                                                                                                                                                                                                                                                                                                                                                                                                   NETIEYINLKKDLGSLSETTEGLKSDLSKYDEAHRKLEDLQSFRSEFLEKKKRKEDLDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQAREEAHRLKCKMKTMEQIELLL---QSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSDYDYLKNELQSKI----NEIDNNNKQIEELESKLRLIEPEIKALEEEINIKENKKD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDET
                                                                                                                                                                                                                                                                              -HLNEELHRLNAQLETIKKYEMELAESQSRKASIEMEVVKLPSIEEELKRLENNAAVVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00470; RecF; 1.
PF02463; SMC_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 20.5
75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  EYENLKEARKATGELADRLK------
                                                                                                                                                                                                                                                372
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                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.48;
                                                                          Last sequence update)
Last annotation updat
                                                                                                          Created)
                                                              non
                                               (Amoeba)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
                                                               muscle.
                                 Acanthamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 176.5; DE Pred. No. 0.049;
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                            update)
                                                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                 KDLVSSRSKL - - - KTLNTELDQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                              446
                                                                                                                                                                                                                                                                                                                                                                                                                                 246
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888 66

81;

Conservative

63;

Mismatches

113;

Indels

73;

Gaps

15;

LAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNA----TVESL

·DADKLEKDLAALKLKILDLEGEKAD------

-LEEDNALLQKKVAGL 931

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Query Match
Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.;

"Complete nuclectide sequence and deduced polypeptide sequence of nonmuscle myosin heavy chain gene from Acanthamoeba: evidence of a hinge in the rodlike tail.";

J. Cell Biol. 105:913-925(1987).

-:- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPA ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

-:- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLE INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALF LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNI
                                                           DOMAIN
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                            NP_BIND
DOMAIN
                                                                                                                                                                                                       DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00063; myosin_head; 1. Pfam; PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                     SMART; SM00015; IQ; I
SMART; SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
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                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                        DOMAI
                                                                                                                                                                                                                                                                               Myosin;
                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A27224; A27224.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y00624; CAA68663.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=87308395;
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                   Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILFIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE MISCELLANDOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 2 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MLC-2).
             Similarity
                                                                                                                                                                                                                                                                                Coiled
                                                                                                                                                                                                                                                                                                                           PD000355; myosin_head;
                                                                                                                                                                                                                                                                                          PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit
                                                            790
848
848
1227
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1253
1483
1483
1483
1489
1766
133
700
1489
1499
                                                                                                                                                                                                                                                                  Alkylation;
                                                                                                                                                                                                                                                                               coil;
                                                                                                                                                                                                                                                                                          IQ;
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1226
1259
1509
1482
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189
682
780
133
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1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             institutions as long
                                                                                                                                                                                                                                                                  Actin-binding; ATP-binding; Calmodulin-binding; ion; Phosphorylation; Multigene family.
             7
24
                                                            171201
            1.5%;
                                                            WW;
            Score
Pred.
                                                                                                                   ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
                                                                                                                                                                                                                              IQ.
COILED COIL
                                                            PHOSPHORYLATION. W; 2CE49BE51173D17E
                                                                                    PHOSPHORYLATION
                                                                                              ALKYLATION (SH-1)
PHOSPHORYLATION.
                                                                                                                                                                    NONHELICAL
                                                                                                                                                                                 ALPHA-HELICAL
                                                                                                                                                                                                                    ALPHA-HELICAL
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            No. 0.
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21-JUL-1986 (Rel. 13, Last sequence update)
10-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Myosin heavy chain, skeletal muscle (Fragments).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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P02562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lu R.C., Wong A.;
"The amino acid sequence and stability predictions of region in myosin subfragment 2.";
J. Biol. Chem. 260:3456-3461(1985).
                                  This
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                                                                                                                                                                                                                                                                                                                                                                   Maeda K., Sczakiel G., Wittinghofer A.; "Characterization of cDNA coding for the complete light meromyosin portion of a rabbit fast skeletal muscle myosin heavy chain."; Eur. J. Biochem. 167:97-102(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myosin.";
Biophys. J. 33:148A-148A(1981).
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Capony J.-P., Elzinga M.;
"The amino acid sequence of A 34,000 dalton fragment
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MEDLINE-85131142; Pu
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                                                                                                                                              FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPETIDES,

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                           SUBFRAGMENT (S2).
SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC
MHICH DICTATE THE ALPHA-HELICAL COILED-COIL:
  European
                SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-JUL-1989
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                                                                                                                                                                                          MYSP_CAEEL P10567;
                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89329036; PubMed=2754733; Schriefer L.A., Waterson R.H.; "Phosphorylation of the N-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kagawa H., Gengyo K., McLachlan A.D., Brenner S., Karn J., "Paramyosin gene (unc-15) of Caenorhabditis elegans. Molecy cloning, nucleotide sequence and models for thick filament
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                               Coiled coil;
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is immodified and this statement is not removed. Usage by and for
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                                                                                                               447
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                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: FOR MOST OF ITS LENGTH, PARRAMYOSIN APPEARS TO FORM AN ALPHA-HELICAL COILED COIL AND SHOWS THE HEPTAD REPEAT OF HYDROPHOBIC AMINO ACID RESIDUES AND THE 28-RESIDUE REPEAT OF CHARGED AMINO ACIDS CHARACTERISTIC OF MYOSIN HEAVY CHAINS. HOWEVER, PARRAMYOSIN DIFFERS FROM MYOSIN IN HAVING NON-HELICAL EXTENSIONS AT BOTH TERMINI AND AN ADDITIONAL "SKIP" RESIDUE THAT INTERRUPTS THE 28-RESIDUE REPEAT. THE DISTRIBUTION OF CHARGED RESIDUES IS ALSO DIFFERENT FROM MYOSIN HEAVY CHAINS.

PTM: PHOSPHORYLATED ON SERINE RESIDUES IN THE NON-ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-TERMINAL REGION
                                                                                                                                                                                                                                                                                                                                                                                      S04027; S04027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its
ETAELEMTVDNLNRANTEAQ---KTTKKQSEQLKTLQASLEDTQRQLQQVLDQYALAQRKV
                          QMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELL---LQSQRSEVEEMIRDMGVGQSAV
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                                                                                                              KLHDELHEAKEALADANRKLHELDLENARLAGEIRELQTALKEADAQRRDAENRAQRALA
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                                                                                                                                                                                      Similarity
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ol. 211:665-665(1990)
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872
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632
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in tail; 1.
protein; Thick filament; Myosin; Phosphorylation
47
NONHELICAL REGION (POTENTIAL).
871
COILED COIL (POTENTIAL).
143
INTERCHAIN (POTENTIAL).
632
INTERCHAIN (POTENTIAL).
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INTERCHAIN (POTENTIAL).
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INTERCHAIN (POTENTIAL).
101949 MW; 894C4BFF4A670C5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            license agreement (See http://www.isb-sib.
                                                                                                                                                                                    7.3%;
21.8%;
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                                                                                                                                                                       65;
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Pred. No. 0.05
65; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CODÓI O.H., PARK C., Itoh K., Adelstein R.S., Beaven M.A.;
Submitted (JUL-1995) to the EMBL/GENBARN/DDBJ databases.
-i-FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS.
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin heavy chain, nonmuscle type A (Cellular myosin type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A).
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                                                                                                     Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
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16-OCT-2001
                              SMART;
                                                           ProDom;
                                                                                    PRINTS;
                                                                                                                                                                                                                  InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                EMBL; U31463; AAA74950.1; -. HSSP; P10587; 1BR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPING.
SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF CHAIN SUBUNITS (MHC), 2 ALKALI LICHT CHAIN SUBUNITS (MLC PROTEIN THE ROBLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPT CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 10 DOMAIN.
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; PR00193; MYOSINHEAVY.
n; PD000355; myosin_head; SM00015; IQ; 1.
; SM00242; MYSC; 1.
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                                                     myosin_head;
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Best Loc
Matches
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P50533;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
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DOMAIN
NP_BIND
DOMAIN
Amphibia; Batrachia; Anura;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
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                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                       Chromosome assembly protein
                                                                                                                                                                                                                                                                                           XENLA
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                                                                                                                                       XCAP-E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKKMEDGVGCLETAEEAKRRLQKDLEGLSQRLEEKVAAYDKLEKTKTRLQQELDDLLVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKKSDDPPGNLEPASATN-----ETVSRLVFESPA---PVEMMNPRLHQPPFGDEIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELKMQLAKKE--EELQAALARVEEEAAQKNMALKKIRELETQISELQEDLESERACRNKA 1130
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654 676
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78 MYOSIN HEAD-LIKE.
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1%; Pred. No. 0.14
112; Mismatches
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COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ACTIN-BINDING.

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

MW; 9B9876D9681FB19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 1617
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                                                                   Mesobatrachia;
                                                                                                                                                         XCAP-E
                                                                                      Craniata; Vertebrata; Euteleostomi;
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                                                                   Pipoidea;
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Best Local S
Matches 73
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InterPro; IPROVISS; SMC_N.
Pfam; PF02483; SMC_N; 1.
Pfam; PF02463; SMC_N; 1.
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Hirano T., Mitchison T.J.;
"A heterodimeric coiled-coil protein required
condensation in vitro.";
Cell 79:449-458(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U13674; AAA64680.1; -. HSSP; P07751; 1AJ3.
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InterPro; IPR003395; SMC_N.
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SUBCELULIAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN
MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND
FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                              EWIASEKHLEG---QANTAYDEKTNNPKEAGQRLHKLQEKKEKLGRNVNMRAMNMLTQAE 996
                                                                                                                                                                               ERYNDLMKRKRIVENDKSKI----LTTIEELDQK 1026
                                                                                                                                                                                                                              SPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEE
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COILED COIL (POTENTIAL).

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ALA/ASP-RICH (DA-BOX).

ALA/ASD-0027DF309 CRC64
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MYH8_HUMAN STANDARD; P13535; Q14910; O1-JAN-1990 (Rel. 13, Created)

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MEDLINE-95324556; PubMed-7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schi Stedman H.H., Rubinstein N.A.;
"Characterization of a human perinatal myosin heavy-chain transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding
Gene 89:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of the human perinatal MHC Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90323631; PubMed-2373371;
Karsch-Mizrachi I., Feghali R., Shows T.B. Jr., Leir
"Generation of a full-length human perinatal myosin
                                                                                                                                                          the
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Eur. J. Biocl
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MEDLINE=95324556; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                          entities requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-46 FROM N.A.
Esser K., Tidhar A., Myszkowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
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"Molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89234168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 860-1937 FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of three
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 502-1937 FROM N.A.
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                                                                                                                                                                                                                                                                                                              SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
ODMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASES ACTIVITY.
MISCELLANBOUS: BACH MYOSIN HEAVY CHAIN (CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED STREED ACCURATE TO THE STREED ACCURATE TO THE SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                   European Bioinformatics Institute. The
by non-profit institutions as long
ified and this statement is not removed.
ities requires a license agreement (See
                                                                                                                                                                                                                                                     SPLIT FURTHER INTO 2
SUBFRAGMENT (S2).
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
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                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
M36769;
Z38133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        perinatal myosin heavy chain.";
ll Biol. 108:1791-1797(1989).
                                                             s requires a license agreement (See an email to license@isb-sib.ch).
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AAC17185.1;
CAA86293.1;
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PubMed=2715179;
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Primates;

    Last sequence update)
    Last annotation update)
    skeletal muscle, perinatal

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1 IQ DOMAIN.
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Catarrhini; Hominidae;
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                                                                                     http://www.isb-sib.ch/announce,
                                                                                                           Usage
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KKLCLERARSPMQNVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNAVLGQK

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IQAALEEAEASLEHEEGKILRIQLELNQVKSEVDRKIAEKDEE

1499

1444

LADRLKK--DLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDDPPGNL ::: | | ::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:: |::: |::: |::: |::: |::: |::: |:: |::: |::: |:: |::: |::: |:: |:

TE--ELEEAKKKLAQRLQEAEEHVEAVNAKCASLEKTKQRLQNEVEDLMLDVERSNAACA

SQRSEVEE - - - - MIRDMGVGQSAVEQLAVYCVSLKKEYENLK - - - - - - -

-EARKATGE

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1443

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ALDKKQRNFDKVLSEWKQK----YEETQAELEASQKESRSLSTELFKVKNVYEESLDQL PASATNETVSRLVFESPAPVEMMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLP

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MOD_RES
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pfam; PF02736; Myosin_N; 1.
pfam; PF01576; Myosin_tail; 1.
pRINTS; PR00193; MYOSINHEAVY.
PTODOm; PD000355; myosin_head;
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InterPro; IPR004009;
InterPro; IPR002928;
  1326
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PIR; A30220;
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                                         115
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                                                                                                                    KKTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEER
                                       NATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQ
                                                                             QQRLINDL---TAQRARLQTEAGEYSRQLDEKDALVSQLSRSKQASTQQTEELKHQLEEE
TKAKNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAIQR
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M35250; AAA36346.1; -
AF067143; AAC21557.1;
A30220; A30220.
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; SM00242; MYSc;
TE; PS50096; IQ;
                                                                                                                                                            l Similarity
77; Conserv
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1847
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658
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132
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698
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19.8%;
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E -> Q (ÎN ŘEF. 1 AND 4).
M -> N (ÎN ŘEF. 3).
N -> H (ÎN ŘEF. 1 AND 4).
NC -> DGG (ÎN ŘEF. 1 AND 4).
E -> G (ÎN ŘEF. 1 AND 4).
E -> Q (ÎN ŘEF. 1 AND 4).
K -> Q (ÎN ŘEF. 1 AND 4).
K -> Q (ÎN ŘEF. 1 AND 4).
E -> D (ÎN ŘEF. 1 AND 4).
                                                                                                                                                              79;
                                                                                                                                                            Score 172.5;
Pred. No. 0.18
79; Mismatches
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METHYLATION (TRI-)
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the Euro
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_HUMAN
                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contenting the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                        Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., "The C terminus of mitosin is essential for its nuclear centromere/kinetochore targeting, and dimerization."; J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95336446; PubMed-7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., C., Novel Cell-cycle-dependent 350-kDa nuclear protein: domain sufficient for nuclear localization.";
Biochem. Biophys. Res. Commun. 212:220-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Breast carcinoma;
MEDLINE-95348175; pubMed-7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.,
"CENP-F is a protein of the nuclear matrix that assemble kinetochores at late G2 and is rapidly degraded after m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CENF_HUMAN STANDARD: PRT; 3210 AA. P49454; Q13246; Q13171; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                      Chan G.K.T., Schaar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain interactions with the kinetochore proteins CENP-F ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95379848; PubMed=7651420; Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., C Jones D., Yang-Feng T.L., Lee W.-H.; The Caracterization of a novel 350-kilodalton nuc that is specifically involved in mitotic-phase Mol. Cell. Biol. 15:5017-5029(1995).
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                                                                                                                                       Cell Biol. 143:49-63(1998).

FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED INTERCOME SEGREGATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROTEIN (RB), CEMP-E AND BUBRI.

SUBUNIT: HOMO- OR HETERODIMER.

SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS), REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.

DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE
                                                        SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
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                 requires a
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ç
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license@isb-sib.ch)
               license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Centromere protein F) (Mitosin)
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01-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4)
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Rhabditidae; Peloderinae;
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EMBL; U30872; AAA82935.1;
EMBL; U25725; AAA86889.1;
HSSP; P02649; 1LE4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                        (MyHC-IIb)
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                                                                                                                                                                                                                                                                                                                                                                                                                              FQNFVSQMKD------KREEASEKRTRKEAEKKAEKEK 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTKFI-QPRDTTIIRPVPVKSKAKSKQKVRIKTVSSASQPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFGDEIDLNTTFDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVLKKVHKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEKTIAQLEIDNSSKSDQIEKLHLRVNDM-----LDQMGTIKDELVKKNEEIKTISAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSEMEKVKHVAENLEAFTSDKDNLLEELESKNKNIEHLKQEIAQLNEKISTKETEKDSE
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1130 AA;
                                                                                                (Rel. 40,
(Rel. 40,
(Rel. 40,
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protein; Coiled coil.
protein; Coiled coil (POTENTIAL).
121 COILED COIL (POTENTIAL).
805 1061 COILED COIL (POTENTIAL).
805 1061 BOFD2EFE3D99FB09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLRKKSDDPPGNLEPASAT --- NETVSRLVFESPAPVEMMNPRLHQ ---- P
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                                                                          chain,
                                                                                                                                                                                                                                                    STANDARD;

    Last sequence update)
    Last annotation update)
    skeletal muscle, fetal (Myosin heavy chain IIb)

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                                                                                                                                                                          Created)
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Pred. No. 0.12
88; Mismatches
                                                                                                                                                                                                                                                    PRT;
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.12;
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Qy Db

115

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A WEDLINE-99318009; runnectives.

A Weiss A., Schlaffino S., Leinwand L.A.;

A Weiss A., Schlaffino S., Leinwand L.A.;

A "Comparative sequence analysis of the complete human sarcomeric myosin are heavy chain family: implications for functional diversity.";

J. Mol. Biol. 290:61-75(1999).

CC -: FUNCTION: MUSCLE CONTRACTION.

CC -: SUBRINIT: MUSCLE CONTRACTION: A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -: SUBRINIT: MUSCLE CONTRACTION: IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -: SUBCELLULAR LOCATION: HICK HIGHLY REPETITIVE, SHOWING CO COMMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CC CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CC CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

CC -: PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC -I- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT OF AMPROMYOSIN (LMM). IT CAN LATER BE APPROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (LMM). TO CAN LATER BE APPROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (LMM). TO CAN LATER BE
                                                                                                                                             ρ
                                                                Matches
                                                                            Query Match
Best Local
                                                                                                                                         DOMAIN
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                  Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_N; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PfINTS; PR00193; MYOSINHEAVY.
PF0D0m; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004009;
InterPro; IPR002928;
InterPro; IPR001609;
                                                                                                                                                                                                                                                                                   SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF111783; HSSP; P08799; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
TISSUE=Skeletal m
1270 QQRLINEL---SAQKARLHTESGEFSRQLDEKDAMVSQLSRGKQAFTQQIEELKRQLEEE 1326
                                                                                                                                                                                                                                      Calmodulin-binding; ATP-binding; Methylation;
                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99318869; PubMed=10388558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                          Myosin;
                                 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HI
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                               KKTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEER 114
                                                               Similarity
78; Conser
                                                                                                                                                                                                                                                          Muscle protein;
                                                                                                                                                                                                                                                                           PS50096;
                                                                                                                                                                                                                          family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000048;
                                                                                                                                             843
179
1939
                                                                                                                                                                                           785
                                                                                                                    784
1939
186
186
223012 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD29949.1;
                                                                                                                                                                                                                                                                       IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               ; IQ.
; myosin_N.
; myosin_tail.
; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             institutions as long
                                                                             7.18;
                                                                                                                                                                                                                                                       Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYOSIN-LIKE GLOBULAR HEAD DOMAIN IQ DOMAIN.
                                                               83;
                                                                                                                                             ATP
MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is not removed.
                                                             Score 170.5;
Pred. No. 0.22
33; Mismatches
                                                                                                                                           COILED COIL (POTENTIAL).
ATP (POTENTIAL).
4W; 40B1AD1D777A47DE CRC64;
                                                                                                                                                                                         MYOSIN HEAD-LIKE IQ.
                                                                               . 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
                                                                                            DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HMM). IT CAN LATER BE NTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                      Alkylation;
                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             уд
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                              1939;
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                                                             Gaps
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RESULT DESCRIPTION OF THE STATE                                                                                                                                                                                                                                                                                                                                                                              Angst B.D., Nilles L.A.,
Structure of the human desmoplakins.
"Structure of plaque.";
the desmosomal plaque.";
raiol. Chem. 265:2603-2612(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESP_HUMAN STANDARD; PRT; 2871 AA.
DESP_HUMAN STANDARD; PRT; 2871 AA.
PI5924; Q14189; O75993; Q9UHN4;
01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen).
                                                                                                                                                                                                                                              Green K.J., Parry D.A.D., Steinert P.M., Virata Angst B.D., Nilles L.A.; J. Biol. Chem. 265:11406-11407(1990).
  "Striate palmoplantar keratoderma resulting haploinsufficiency.";
J. Invest. Dermatol. 113:940-946(1999).
[6]
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                                                                                                   Whittock N.V., Ashton G.H., Keane F.M., Eady R.A.J., Mc
                                                                                                                                                   MEDLINE=20062965;
                                                                                                                                                                                                   SEQUENCE OF 2854-2871 FROM N.A.
                                                                                                                                                                                                                                                                                                                        MEDLINE=90361712; PubMed=2391353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green K.J., Parry D.A.D., Steinert P.M., Virata M.L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Foreskin;
MEDLINE-90153880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92115697; PubMed=1731325;
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                                                                                                                                                     PubMed-10594734;
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                                                                                                   H., Dopping-Hepenstal P.J.,
McGrath J.A.;
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desmoplakin I
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                                                                            from desmoplakin
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HSSP; P01100; 1FOS.
MIM; 125647; -.
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"The amino-terminal domain of desmoplakin binds to plakoglobin clusters desmosomal cadherin-plakoglobin complexes.";
J. Cell Biol. 139:773-784(1997).

-i- FUNCTION: MAJOR HIGH MOLECULAR WEIGHT PROTEIN OF DESMOSOMES.
INVOLVED IN THE ORGANIZATION OF THE DESMOSOMAL CADHERIN-PLAKOGLOBIN COMPLEXES INTO DISCRETE PLASMA MEMBRANE DOMAINS
THE ANCHORING OF INTERMEDIATE FILAMENTS TO THE DESMOSOMES.
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EMBL; AL031058; CAA19927.1; --
EMBL; J05211; AAA53766.1; --
EMBL; AF139065; AAF19785.1; --
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InterPro; IPR002017; Spectrin.
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SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
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STRATIFED ORIGIN.

STRATIFED ORIGIN.

DOMAIN: THE N-TERMINAL REGION IS REQUIRED FOR LOCALIZATION
DESMOSOMAL PLAQUE AND INTERACTS WITH THE N-TERMINAL REGION
DESMOSOMAL PLAQUE AND INTERACTS WITH INTERME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: INNERMOST PORTION OF THE DESMOSOMAL PLAQUE
ALTERNATIVE PRODUCTS: 2 ISOFORMS; DPI/DP1 (SHOWN HERE) AND
DPII/DP2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: DPI IS APPARENTLY AN OBLIGATE CONSTITUENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: DEFECTS IN DSP ARE A CAUSE OF STRIATE PALMOPLANTAR
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RESULT 28
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Matches
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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                                                                                                                                                                                                                                                 QLYECQLIDKTTLDKLLKGKKSV--EEVASEIQPFL
                                                                                                                                                                                                                                                                       QPRDTTIIRPVPVKSKAKSKQKVRIKTVSSASQPKL
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                                                                                                                                                                                                                                                                                                                                                                      TSGSQHCLPKKLCLERARSP-------MQNVLKKVHK------VSKPESQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                              ELRSQLQISNNRTLELQGLINDLQRERENLRQEIEKFQKQALEASNRIQESKNQCTQVVQ
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                                                                                                                                                                                                                                                                                                                                                                                             ERESLLVKIKVLEQDKARLQRLEDELNRAKSTLEAETRVKQRLECEKQQIQNDLNQWKTQ
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)3; Conservative
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1195
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2871
                                                                                                          (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
modulatory factor (TMF).
                                                                   (Human).
letazoa; Chordata;
ltheria; Primates;
                                                                                                                                                                                  STANDARD;
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1794
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2688
A; 331771
           PubMed=1409643;
                                   AND FUNCTION
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18.0%;
Wu F.,
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MISSING (IN ISOFORM E
R -> A (IN REF. 2).
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SV -> RL (IN REF. 2).
SW -> RG (IN REF. 2).
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PLECTIN 16.
PLECTIN 17.
6 X 4 AA TANDEM I
INTERACTS WITH PI
PLAKOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 170.5; D
Pred. No. 0.34;
0; Mismatches
                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                    PRT;
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 Lusis
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A.J.,
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                                                                        Hominidae;
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Sparkes
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DPII).
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R.S.,
                                                                                    Euteleostomi;
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AND JUNCTION
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RESULT 29
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Best Local
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                                          HIP1_HUMAN S
000291; 000328;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
16-OCT-2001 (Rel
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DOMAIN
SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 89:9372-9376(1992).
-!- FUNCTION: THIS PROTEIN BINDS THE HIV-1 TATA ELEMENT TRANSCRIPTIONAL ACTIVATION BY THE TATA-BINDING PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L01042; AAD54608.1; MIM; 601126; -.
                           Huntingtin
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                                                                                                                                                                                                                                                                                                              LSDRLGESQTLLAAAVERERAATEELLANKIQMSSMESQNSLLRQENSRFQAQLESE---
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                                                                                                                                                                                     ERKKAIFTQETIKEKERKPFSVSSTPTMSRSSSISGVDMAGLQTSFLSQ
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07; Conservative
                                                                                                                                                                                                                                                                                                                                          -----CLERARSPMQNVLKKVHKVSKPESQLSLGGQ---RCVGELDEELAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ion regulation; DNA-binding; Repressor; Coiled 439 922 COILED COIL (POTENTIAL). 984 1092 COILED COIL (POTENTIAL). 1093 AA; 123170 MW; 26133E8E5F4677BE CRC64;
                             interacting
                                                                                                                                                                                                                                                 -KNRLCKLEDENNRYQVELENLKDEYVRTLEETRKEKTLLNSQLE--MERMKVEQ
                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                          STANDARD;
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                           Last annotation update)
protein 1 (HIP-I) (Fragment).
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HIP1

sapiens

(Human)

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EMBL;
EMBL;
EMBL;
EMBL;
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Bradshaw
                                                                                                                                                                                    entities
                                                                                                                                                                                                                          use
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                                                                                                                                                                                                         modified
                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wanker E.E., Rovira C., Scherzinger E., Tait D., Colicelli J., Lehrach H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97227296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 82-995 FROM MEDLINE-97285121; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic organization of the human HIP1 gene and its candidate gene in a family diagnosed with Huntington
                                                                                                                                                                   send
                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resta
                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: CYTOPLASMIC, MEMBRANE-ASSOCIATED PROTEIN.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HIP1-1 AND HIP1-2; ARE PRODUCED
BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED WITH THE HIGHEST LEVEL
                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIP1 INTERACTION IS INVERSELY CORRELATED TO THE LENGHT OF THE POLYGLUTAMINE TRACT ADDED TO THE HUNTINGTIN PROTEIN IN HUNTINGTON
                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SLA2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: BINDS HUNTINGTIN. THIS INTERACTION
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                 AF052288;
AF052261;
AF052262;
AF052263;
AF052264;
AF052265;
AF052266;
                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                                                                                                                                                   non-profit institu
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H., Hinds K., Harri
d (APR-1998) to the
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Pfam; PF01608; I_LWEQ; 1.
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                              NVLKKVHKVSKPESQLSLG---GQRCVGEL-DEELAGAFPLFIRNAVLGQKQPNRTTAES
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 RSSTDVVRIGFDG--LGGRTKFIQPRDTTIIRPVPVKSKAKSKQKVRIKTVSSASQPK
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                     NCLSKIKAIG--
                                                               LAHLTSDAIAHGATTCLRAPPEPADSLTEACKQYGRETLAYLASLEEEGSLENADSTAMR
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TALIN-LIKE.
KLHSCLP -> EFAAAST (IN REF. LNQLEE -> STRPRI (IN REF. 4
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-!- SIMILARITY: TO YEAST YHL010C AND S.POMBE SPAC16E8.13
-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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01-NOV-1997 (Rel. 35, 1
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14-pothetical 141.2 kba
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SMART; SM00290; ZnE_UBP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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InterPro; IPR001841; Znf_ring.
InterPro; IPR001607; zf_UBP.
Pfam; PF00069; pkinase; 2.
Pfam; PF00097; zf_C3HC4; 1.
Pfam; PF020148; zf_UBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chissoe
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Rhabditidae; Peloder
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Q09298;
                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                       LSLCTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTCPQCR---------
LRHDMEQTMSKMEKTAYAQVENLEHQLTER----STELKSLKGDLDDTVTARKVAE- 1125
                                                                                                               NDCGMSNDLWICLICGNIGCGRYAEQHAQRHWELTSHTYSLKVGGERV-----WDYAGDN
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                         IIDTLRDTLEERNAT ---- VESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR
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E; PS50089; ZF_RING_2; 1.

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etical protein; Zinc-finger.

718 945 RING-TYPE.

748 751 POLY-SER.

124 1229 POLY-SER.

1235 1238 POLY-LYS.

1235 1238 POLY-LYS.

1238 AA; 141212 MW; 589A6E0:
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Inae; Caenorhabditis.
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a protein EEED8.9 in chr
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MYSS_CYPCA
                                                                                                                                                                                              RT different primary structures in carp fast skeletal muscle.";

RE Biochem. Biophys. Res. Commun. 208:118-125(1995).

C: i- FUNCTION: MUSCLE CONTRACTION.

C: -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C: -SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C: -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN SUBUNITS (MLC)

CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAPEDTIDES,

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAPEDTIDES,

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAPEDTIDES,

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEDTAPEDTIDES,

CC CYCLES OF A 28-RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REGUIRED FOR MYOSIN ATPASE ACTIVITY.

CC MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MERCMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

CC STILTERS AND AND AND A GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1182
                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watabe S., Imai J., Nakaya M., Hirayama Y., Okamot
Uozumi T., Hirono I., Aoki T.;
"Temperature acclimation induces light meromyosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acclimation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural differences in the crossbridge head of temperature-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last annotation upo
Myosin heavy chain, fast skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95194396; PubMed=7887920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1387-1528 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle and their gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97176447; PubMed=9023993;
Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"CDNA Cloning of myosin heavy chain isoforms from carp fast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 981-1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fast muscle;
MEDLINE=97352533; Pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215
                                                                                                                                      SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDLQSQVNDLLMH--FETQNKLK---EQLDAGKITQEEITESQVELDSSSSSSRKLNRK 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KRATQTNEKVNKLANELKDER-EINQMLRKDQQVWKGQVEKLIESQKTARTEYE--KKI 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKCKMKTMEQIELL - - - LQSQRSEVEEMIR - DMGVGQSAVEQLAVYCVSLKKEYENLKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200:27-34(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246:380-387(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subfragment-1 isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9208928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                          There are no rest
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                               ne EMBL out
restrictions c
rat is in
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                                                                                         a collaboration
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                                                                                       outstation
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entities modified

non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).

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Best Local S
Matches 97
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Pfam; PF00736; Myosin_head; 1.
Pfam; PF02736; Myosin_kil; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PFCDOM; PD000355; MYOSIN_head; 1
SMART; SM0015; IQ; 1.
SMART; SM0016; IQ; 1.
PROSITE; PS50096; IQ; 1.
PROSITE; PS50096; IQ; 1.
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Multigene famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                     399
                                                                                                             301
                                                                                                                                                                                                                                             173
                                                                                                                                                                                                                                                                                       135
                                                                                                                                                       258
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Q-STLDSEVRSRNDALRV
                    QPNRTTAESRSSTDVVRI
                                          TALEEAEGTLEHEESKILRVQLELNQVKSEIDRKLAEKDEEM----EQIKRNSQRVIDSM 1598
                                                                                                                               VERANSLAANLDKKQRNFDKVLAEWKQKYEESQAELEGAQKEARSLSTELFKMKNSYEEA
                                                                                                                                                                                                                                                                                                                               VKAQLSQK-----
                                                               LCLERARSPMONVLKKVHKVSKPESQLSLGGQRCVGELDEELAGAFPLFIRNA--VLGQK
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D50476;
D43700;
P08799;
                                                                                      LDHLETLKRENKNLQQ----
                                                                                                                                                                          RTKYETDAIQRTEELEEAKKKLAQRLQDAEESIEAVNSKCASLEKTKQRLQGEVEDLMID
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                                                                                                                                                                                                                                                                                   LKKQMKFLEQRQDETKQAREEAHRLKCKMKT-----MEQIELL------
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812
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659
761
129
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                                                                                                       -MMNPRLHQPPFGDEIDLNTTFDVNTPPTQTSGSQHCLPK------K
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BAA09069.1;
BAA07802.1;
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811
839
1935
185
681
775
129
                                                                                                                                                                                              ----RLKKDLVSSRSKLKTLNTE----LDQAKLELRSAQKDL---
                                                                                                                                             -QSADQEITSLRKKSDDPPGNLEPASATNETVSRLVFESPAPVE--
                                                                                                                                                                                                                                                                                                                                                                                                        7.18;
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                                                                                      -EIS----
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                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                             Score 169; DB
Pred. No. 0.26,
90; Mismatches
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
MW; 9A1244B67D63C83B (
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HINGE.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
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IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coil; Thick filament; Actin-binding
                                                                                     DLTEQLGETGKSIHELEKAKKTVESEKSEIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                         DB
. 26;
                                                                                                                                                                                                                                                                                                                                                                                              173;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                              Indels 138;
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ALD CONTRACTOR OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
MYH9_CHICK
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001699; myosin_head.
Pfam; PP00612; IQ; 1.
Pfam; PP000613; myosin_head; 1.
Pfam; PP002736; Myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                           Myosin;
Coiled o
                                                                                             DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                  Prodom; PD000355; myosin horsesmart; Smoore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellular myosin.";
Proc. Natl. Acad. Sci. U.S.A. 86:7726-7730(1989).
-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYH9_CHICK STANDARD; PRT; 1959 AA. P14105; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) MYOSIN heavy chain, nonmuscle (Cellular myosin MYH9.
                                                                                                                                                                                                                                                            SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                             DOMAIN
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P10587; 18R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M26510; AAA48974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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MEDLINE-90046668; PubMed-2813355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adelstein R.S.; "Cloning of the cDNA encoding the myosin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shohet R.V., Conti M.A., Kawamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITI CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPING. SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL SHAPE, AND
                                                                                                                                                                                           coil;
                                                                                                                                                                                                     ; PS50096; IQ; 1.
ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000048; IQ.
                        779
837
174
654
694
704
                                                                                                                                                                                         Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
  ₹,
                        778
808
1925
181
676
694
704
                                                                                                                                                                                                                                                                                                          myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIALIZED FUNCTIONS SUCH AS SECRETION
    226502
                                                                                                                                                                                           Multigene fami
    ₹
                                                                                        IQ.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
                     ACTIN-BINDING.
ALKYLATION (SH-1) (POTENTIAL)
ALKYLATION (SH-2) (POTENTIAL)
                                                                                                                                                                   NISOYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s.
                                                                                                                                                                   HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence up
16-0CT-2001 (Rel. 40, Last annotation
Protein CXorf5 (Protein 71-7A).
                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-98390187; PubMed-9722947;
de Conciliis L., Marchitiello A., Wape
Giglio S., Mariani M., Consalez G.G.,
Ballabio A., Banfi S.;
                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1131
  This
                          Genomics 51:243-250(1998).

- I- ALTERNATIVE PRODUCTS: 2 ISOFORMS;
- PRODUCED BY ALTERNATIVE SPLICING.
- I- TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                     HUMAN
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                                                                                            "Characterization of Cxorf5
Xp22 and encoding a protein
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 SWISS-PROT entry is copyright. It
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MYH2_HUMAN STANUTHUMAN STANUTHUMAN STANUTHUMAN STANUTHUMAN OPUKX2; Q16229; Q14322; Q160CT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation heavy chain, skeletal muscle, &

update) on update) , adult 2

(Myosin

heavy chain

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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

MYH2 OR MYHSA2

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MYH2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
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MISSING (IN ISOFORM 2).
MW; C2BF4376F89E6738 CRC64;
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RA Ennion S., Sant'ana Pereira J., Sargeant T., Young A., Goldspink G.;

RT "Characterization of human skeletal muscle fibres according to the myosin heavy chains they express";

RL J. Muscle Res. Cell Motil. 16:35-43(1995).

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

CC CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

CC CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILS.

CC -!- FIM: TWO CYSTEINE RESUDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC ALKYLATED AND ARE REGUIRED FOR MYOSIN GAN BE SPLIT INTO 1 LIGHT CREATED AND ARE REGUIRED FOR MYOSIN CAN BE SPLIT INTO 1 LIGHT CREATED AND ARE REGUIRED FOR MYOSIN CAN BE SPLIT INTO 1 LIGHT CREATED AND ARE REGUIRED FOR MYOSIN CAN BE SPLIT INTO 1 LIGHT CREATED AND ARE REGUIRED FOR MYOSIN CAN BE SPLIT INTO 1 LIGHT CREATED AND AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED CREATED AND ALTER BE SUBFRAGMENT (S2).

CC -!- SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                   Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1
SMART; SM00015; MYSC; 1.
SMART; SM00242; MYSC; 1.
                PROSITE; PSOUCCE, MVOSin; Muscle protein;
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                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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          Calmodulin-binding; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Type IIx myosin heavy chain transcripts fibers of human skeletal muscle."; Am. J. Physiol. 267:C1723-C1728(1994).
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InterPro; IPR002928;
                                                                                                                                                                                                                                                                                            InterPro; IPR000048;
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                                                                                                                                                                                                             PF00612; IQ;
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              Methylation;
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SEQUENCE
                                                                   Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T., Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.; "Tpr, a large coiled coil protein whose amino terminus is involved activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex."; J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                         Mitchell P.J., Cooper C.S.;
"The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain.";
Oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
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MEDLINE=93064711; PubMed=1437155;
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TISSUE SPECIFICITY: HIGHEST IN TESTIS,
BRAIN, LOWER LEVELS IN HEART, LIVER, A
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                                                                                                                                                           Query Match
Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meier I., Phelan T., Gruissem W., Spiker S., Schneider D.
"MFP1, a novel plant filament-like protein with affinity
attachment region DNA."
Plant Cell 8:2105-2115(1996).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. VFNT CHERRY; TISSUE-Fruit;
MEDLINE-97112038; PubMed-8953774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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            QSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSR
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                                         LEREVSKLQ---
                                                                     RNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLL
                                                                                                  LIADLTREKENLRRMVDAELDNVNKLKQEIEVTQESLENSRSEVSDITVQLEQLRDLSSK
                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    697 AA;
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filament-like protein 1.
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01-FEB-1996 (Rel. 33, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Myosin heavy chain, smooth muscle isof
                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Cnoruaca; Claulaca, Chammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                       InterPro; IPR001609;
                                                                                                                                             InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                          HSSP; P08799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92073350; PubMed=1961735; Babij P., Kelly C., Periasamy M.; "Characterization of a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P35748
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5' end of the gene.";
c. Natl. Acad. Sci. U.S.A. 88:10676-10680(1991).
FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
AND 2 REGULATORY LIGHT CHAIN SUBUNITS of the myofibrils.
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLAYED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
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   PF00612;
PF00063;
PF02736;
PF01576;
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                                                                                                                                                                                                                                                                                                                              M77812; AAA31395.1;
                                                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch)
                                                                                                                                                                                                                                            IPR000048; IQ
; myosin_head;
; myosin_N; 1.
; myosin_tail;
                                                                                                                                                                                                                                                                             1MMD
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                                                                                                                                                                                                                                                                                                                                                                                                                    license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ), Last annotation update) smooth muscle isoform (SMMHC).
                                                                                                                    myosin_head.
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Best Local
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MAR binding filament-like protein 1.
MFP1 OR AT3G16000 OR MSL1.4.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
               DNA Res. 7:131-135(2000).

-!- FUNCTION: BINDS DNA. INTERACTS WITH CHROMATIN VIA MATRIX ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NUCLEAR ARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR MATRIX
                                                                                                                     STRAIN=CV. Columbia;
MEDLINE=20277480; PubMed=10819329;
MEDLINE=20277480; PubMed=10819329;
Saturctural analysis of Arabidopsis thaliana chromosome 3. I. features of the regions of 4,504,864 bp covered by sixty Pl an clones.";
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SMART; SM00242; MYSC; 1.
SMART; SM00242; MYSC; 1.
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Calmodulin binding; ATP-binding; Methylation; Alkylation;
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-83273600; PubMed-6576334;
Karn J., Brenner S., Barnett L.;
Protein structural domains in the Caenorhabditis elegans
"Protein structural domains in the Caenorhabditis elegans
"Protein structural domains in the Caenorhabditis elegans
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P02566;
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                                                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Pelodei
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22 35 POLY-SER.
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Pred. No. 0.11;
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-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAR PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERAGMENTS (S1) AND 1 ROD-SHAPED
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DOMAIN
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MCIachlan A.D., Karn J.;
"Periodic charge distributions in the "Periodic charge distributions in muscle
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pfam; PF02736; Myosin_N; 1.
pfam; PF01576; Myosin_tall; 1.
print; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J01050; AAA28124.1; -. EMBL; V01494; CAA24738.1; -. EMBL; A02992; MWKW.
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MEDLINE=82272395;
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ATP-binding;
                                                                                                                                                                                                                                                                                                                              SMART;
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InterPro; IPR002928;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY C.ELEGANS.
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an email to license@isb-sib.ch).
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; PubMed=6571695;
and R.F., Karn J.,
                       1880
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PubMed=7202124;
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Myosin_tail
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ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING (TRI-) (PO
ALKYLATION (SH-1).
ALKYLATION (SH-2).
E -> R (IN REF. 2).
I -> L (IN REF. 2).
MW; B66F0BB2FE27B67F C
      MW.
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ed transfer RNA.";
                                                                                                                                                                                                                       MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL)
ALPHA-HELICAL TAILPIECE
                                                                                                                                                               ATP (BY SIMILARITY).
                                                                                                                                                                                    LIGHT MEROMYOSIN (LMM)
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Best Local Similarity
J.
[4]
            SEQUENCE OF 1-203.

MEDLINE-88032919; PubMed-3312184;

Maita T., Onishi H., Yajima E., Matsuda G.;

"Amino acid sequence of the amino-terminal heavy chain of chicken gizzard myosin.";

J. Biochem. 102:133-145(1987).
                                                                                                                                            "Complete primary structure of vertebrate smooth muscle myosin chain deduced from its complementary DNA sequence. Implications topography and function of myosin.";
J. Mol. Biol. 198:143-157(1987).
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88118918; PubMed-2892941;
Yanagisawa M., Hamada Y., Katsura
                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11,
15-DEC-1998 (Rel. 37,
16-OCT-2001 (Rel. 40,
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                                                                                                           Masaki T.
                                                                                                                        REVISIONS
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                                                                                                                                                                                                                                                                                Archosauria;
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pfam; pF02736; Myosin_N; 1.
pfam; pF01576; Myosin_tail; 1.
pRINTS; pR00193; MYOSINHEAVY;
proDom; pD000355; myosin_head;
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PIR; S
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SMART; SM00242; MYSC;
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                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAR PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLARDOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS SIMILARITY: CONTAINS
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SIMILARITY: CONT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S03166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1BR1; 09-SEP-98.
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profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myosin_head
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  MISSING (IN REF. 3).
KDTSITQGPSFS -> RTPASLKVHLFP
W; B7B6C923E5273D93 CRC64;
                                                                  ALKYLATION (SH-1)
ALKYLATION (SH-2)
                                                                                                                                       BLOCKED.
                                                                                                              METHYLATION (TRI-)
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                                                                                                                                                                                                                            COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                     RODLIKE
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light chain: visualization
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MBL outstation -
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Query Match Best Local Similarity

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                                                                         1356 QLDEEV 1361
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                                                                                                                                                           317 LNTTEDVNTPPTQTSGSQHCLPKKLCLERARSPMQNVLKKVHKVSKPESQLSLGGQRCVG 376
                                                                                                         377 ELDEEL 382
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